

# SEQUENCE LISTING

<110> Godfrey, Wayne  
Buck, David  
Engleman, Edgar G.

<120> Receptor on the Surface of Activated T-Cells: ACT-4

<130> 16524.010

<150> US 08/472,940

<151> 1995-06-06

<150> US 08/147,784

<151> 1993-11-03

<160> 2

<210> 1

<211> 1058

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (15)..(845)

<220>

<223> ACT-4-h-1 cDNA

<400> 1

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		Met	Cys	Val	Gly	Ala	Arg	Arg	Leu	Gly	Arg	Gly	Pro			
		1				5					10					
tgt	gcg	gct	ctg	ctc	ctc	ctg	ggc	ctg	ggg	ctg	agc	acc	gtg	acg	ggg	98
Cys	Ala	Ala	Leu	Leu	Leu	Leu	Gly	Leu	Gly	Leu	Ser	Thr	Val	Thr	Gly	
		15					20					25				
ctc	cac	tgt	gtc	ggg	gac	acc	tac	ccc	agc	aac	gac	cgg	tgc	tgc	cac	146
Leu	His	Cys	Val	Gly	Asp	Thr	Tyr	Pro	Ser	Asn	Asp	Arg	Cys	Cys	His	
		30				35					40					
gag	tgc	agg	cca	ggc	aac	ggg	atg	gtg	agc	cgc	tgc	agc	cgc	tcc	cag	194
Glu	Cys	Arg	Pro	Gly	Asn	Gly	Met	Val	Ser	Arg	Cys	Ser	Arg	Ser	Gln	
		45			50					55					60	
aac	acg	gtg	tgc	cgt	ccg	tgc	ggg	ccg	ggc	ttc	tac	aac	gac	gtg	gtc	242
Asn	Thr	Val	Cys	Arg	Pro	Cys	Gly	Pro	Gly	Phe	Tyr	Asn	Asp	Val	Val	
				65					70					75		
agc	tcc	aag	ccg	tgc	aag	ccc	tgc	acg	tgg	tgt	aac	ctc	aga	agt	ggg	290
Ser	Ser	Lys	Pro	Cys	Lys	Pro	Cys	Thr	Trp	Cys	Asn	Leu	Arg	Ser	Gly	
			80					85					90			
agt	gag	cgg	aag	cag	ctg	tgc	acg	gcc	aca	cag	gac	aca	gtc	tgc	cgc	338

10750-5182550

Ser Glu Arg Lys Gln Leu Cys Thr Ala Thr Gln Asp Thr Val Cys Arg	
95 100 105	
tgc cgg gcg ggc acc cag ccc ctg gac agc tac aag cct gga gtt gac	386
Cys Arg Ala Gly Thr Gln Pro Leu Asp Ser Tyr Lys Pro Gly Val Asp	
110 115 120	
tgt gcc ccc tgc cct cca ggg cac ttc ttc cca ggc gac aac cag gcc	434
Cys Ala Pro Cys Pro Pro Gly His Phe Ser Pro Gly Asp Asn Gln Ala	
125 130 135 140	
tgc aag ccc tgg acc aac tgc acc ttg gct ggg aag cac acc ctg cag	482
Cys Lys Pro Trp Thr Asn Cys Thr Leu Ala Gly Lys His Thr Leu Gln	
145 150 155	
ccg gcc agc aat agc tcg gac gca atc tgt gag gac agg gac ccc cca	530
Pro Ala Ser Asn Ser Ser Asp Ala Ile Cys Glu Asp Arg Asp Pro Pro	
160 165 170	
gcc acg cag ccc cag gag acc cag ggc ccc ccg gcc agg ccc atc act	578
Ala Thr Gln Pro Gln Glu Thr Gln Gly Pro Pro Ala Arg Pro Ile Thr	
175 180 185	
gtc cag ccc act gaa gcc tgg ccc aga acc tca cag gga ccc tcc acc	626
Val Gln Pro Thr Glu Ala Trp Pro Arg Thr Ser Gln Gly Pro Ser Thr	
190 195 200	
cgg ccc gtg gag gtc ccc ggg ggc cgt gcg gtt gcc gcc atc ctg ggc	674
Arg Pro Val Glu Val Pro Gly Gly Arg Ala Val Ala Ala Ile Leu Gly	
205 210 215 220	
ctg ggc ctg gtg ctg ggg ctg ctg ggc ccc ctg gcc atc ctg ctg gcc	722
Leu Gly Leu Val Leu Gly Leu Leu Gly Pro Leu Ala Ile Leu Leu Ala	
225 230 235	
ctg tac ctg ctc cgg agg gac cag agg ctg ccc ccc gat gcc cac aag	770
Leu Tyr Leu Leu Arg Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys	
240 245 250	
ccc cct ggg gga ggc agt ttc cgg acc ccc atc caa gag gag cag gcc	818
Pro Pro Gly Gly Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala	
255 260 265	
gac gcc cac tcc acc ctg gcc aag atc tgaccttgggc ccaccaaggt	866
Asp Ala His Ser Thr Leu Ala Lys Ile	
270 275	
ggacgctggg ccccgccagg ctggagcccg gagggctctgc tgggcgagca gggcaggtgc	926
aggccgcctg ccccgccacg ctctggggcc aactctgcac cgttctaggt gccgatggct	986
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aaaccttggc ag	1058

<211> 277  
<212> PRT  
<213> Homo sapiens

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<223> deduced amino acid sequence of ACT-4-h-1

<400> 2

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Leu Leu Leu Gly Leu Gly Leu Ser Thr Val Thr Gly Leu His Cys Val  
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Gly Asp Thr Tyr Pro Ser Asn Asp Arg Cys Cys His Glu Cys Arg Pro  
35 40 45

Gly Asn Gly Met Val Ser Arg Cys Ser Arg Ser Gln Asn Thr Val Cys  
50 55 60

Arg Pro Cys Gly Pro Gly Phe Tyr Asn Asp Val Val Ser Ser Lys Pro  
65 70 75 80

Cys Lys Pro Cys Thr Trp Cys Asn Leu Arg Ser Gly Ser Glu Arg Lys  
85 90 95

Gln Leu Cys Thr Ala Thr Gln Asp Thr Val Cys Arg Cys Arg Ala Gly  
100 105 110

Thr Gln Pro Leu Asp Ser Tyr Lys Pro Gly Val Asp Cys Ala Pro Cys  
115 120 125

Pro Pro Gly His Phe Ser Pro Gly Asp Asn Gln Ala Cys Lys Pro Trp  
130 135 140

Thr Asn Cys Thr Leu Ala Gly Lys His Thr Leu Gln Pro Ala Ser Asn  
145 150 155 160

Ser Ser Asp Ala Ile Cys Glu Asp Arg Asp Pro Pro Ala Thr Gln Pro  
165 170 175

Gln Glu Thr Gln Gly Pro Pro Ala Arg Pro Ile Thr Val Gln Pro Thr  
180 185 190

Glu Ala Trp Pro Arg Thr Ser Gln Gly Pro Ser Thr Arg Pro Val Glu  
195 200 205

Val Pro Gly Gly Arg Ala Val Ala Ala Ile Leu Gly Leu Gly Leu Val  
210 215 220

Leu Gly Leu Leu Gly Pro Leu Ala Ile Leu Leu Ala Leu Tyr Leu Leu  
225 230 235 240

Arg Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly  
245 250 255

TOP SECRET

Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser  
260 265 270

Thr Leu Ala Lys Ile  
275

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